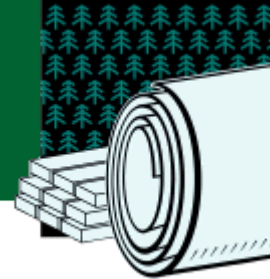


FOREST PRODUCTS

Project Fact Sheet



SEARCH FOR MAJOR GENES USING PROGENY TEST DATA TO ACCELERATE THE DEVELOPMENT OF GENETICALLY SUPERIOR LOBLOLLY PINES

BENEFITS

- Takes advantage of available breeding materials and genetic test information
- Identifies major segregating genes with economic value
- Helps tree breeders make effective decisions on managing stock
- Enhances forest productivity
- Reduces time and cost for QTL detection
- Transfers information to conventional loblolly pine breeding program

Forest Genetics, Statistics, and Biotechnology Will All Be Focused on Improving U.S. Forest Resources

The North Carolina State University–Industry Cooperative Tree Improvement Program has spent more than 40 years using traditional breeding, testing, and selection methods to improve the genetics of loblolly pines on large plantations. Recent developments in molecular biology and genomic mapping suggest novel approaches to accelerate the detection of genes for such desirable traits as rapid growth, resistance to disease and insects, and certain wood properties.

Researchers will couple the extensive breeding materials and progeny test datasets available through the Tree Improvement Program with genetic modeling and marker analysis, to screen for economically important genes. Analysis of the datasets already on hand is expected to reveal quantitative trait loci (QTLs) more quickly than by conventional methods, and at a lower cost. After the genes are detected, and confirmed with molecular markers, new forestry breeding strategies can be developed that yield superior strains of loblolly pine.

APPLICATIONS

The application of genetic findings to tree breeding programs is expected to significantly increase productivity in industrial tree programs.

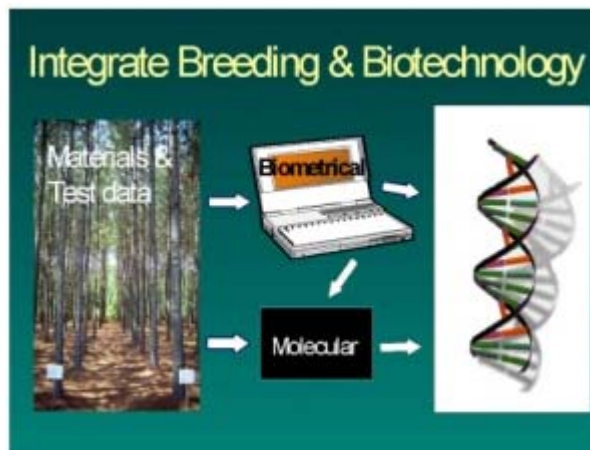


Figure 1. Researchers will use extensive breeding materials and progeny test datasets for quantitative genetic modeling and molecular marker analysis to screen for economically important genes in loblolly pine.

OFFICE OF INDUSTRIAL TECHNOLOGIES

ENERGY EFFICIENCY AND RENEWABLE ENERGY • U.S. DEPARTMENT OF ENERGY

PROJECT DESCRIPTION

Goal: To develop models for detecting major genes and statistical methods and computer software for screening progeny test data, to confirm major gene segregation with molecular markers, and to develop strategies for marker-assisted breeding.

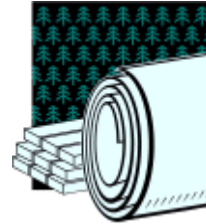
Of the more than 10,000 crosses made by the Tree Improvement Cooperative, skewed distributions on the plots of six-year tree heights will be examined more closely to detect potential genetic effects. Genetic models and new analytical methods (and software) will be developed that are suitable for gene detection and QTL mapping in tree breeding pedigrees. The purpose is to identify families that carry one or more genes for traits such as growth, stem straightness, and rust resistance.

Needles from 500 trees that were the offspring of four different crosses were found to contain different combinations of two major genes. After further study, the needles will be used to construct a genomic map. DNA will be extracted and about 300 genetic markers obtained to map the predicted genes for each of the 500 trees. To analyze QTLs and validate the marker and trait association, regression, interval mapping, and composite interval mapping will be carried out. When the major genes are identified and mapped for the four families, genotypes of the DNA markers on each side of the major genes will also be obtained to confirm the genetic models.

The results of these studies will be applied to developing new strategies to manage tree-breeding programs. When the parental genotypes are known, methods for future line breeding can be worked out.

PROGRESS & MILESTONES

- A computer program for a 2-locus genetic model was developed to describe the differences in means and variances of the data from the 10,000 crosses made by the Tree Improvement Cooperative.
- Forty genetic markers were obtained for one of the four families involved in the study of tree needles; one marker is associated with six-year tree height and can explain 10 percent of variation within the family.
- The Forest Biotechnology Group at North Carolina State University has the tools in place to use various marker systems.



PROJECT PARTNERS

North Carolina State University
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Bowater, Inc.
Cataba, SC

Champion International Corp.
Cantonment, FL

International Paper Company
Bainbridge, GA

Mead Coated Board
Phenix City, AL

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